## DSP-14

GGCCAGTGGGGGTGGCTGCGGCTGCTACATGCCCCACGGACCAGAACCTCCCGACGCGGCCAGGCCCCGGC ACACCCAGCTGCAGAAAGGAGAGAAAATCCCTTGGCTCTAAAATGACATCTGGAGAAGTGAAGACAAGCCTCAAGAA TGCCTACTCATCTGCCAAGAGGCTGTCGCCGAAGATGGAGGAGGAGGAGGAGGAGGAGGACTACTGCACCCCTGGAG CCTTTGAGCTGGAGCGGCTCTTCTGGAAGGGCAGTCCCCAGTACACCCACGTCAACGAGGTCTGGCCCAAGCTCTAC CGGCCGCTGGAACGTGGACACTGGGCCCGACTACTACCGCGACATGGACATCCAGTACCACGGCGTGGAGGCCGACG ACCTGCCCACCTTCGACCTCAGTGTCTTCTTCTACCCGGCGGCAGCCTTCATCGACAGAGCGCTAAGCGACGACCAC AGTAAGATCCTGGTTCACTGCGTCATGGGCCGCAGCCGGTCAGCCACCCTGGTCCTGGCCTACCTGATGATCCACAA GGACATGACCCTGGTGGACGCCATCCAGCAAGTGGCCAAGAACCGCTGCGTCCTCCCGAACCGGGGCTTTTTGAAGC AGCTCCGGGAGCTGGACAAGCAGCTGGTGCAGCAGAGGCGACGGTCCCAGCGCCCAGGACGGTGAGGAGGAGGATGGC  ${\tt AGGGAGCTG}$ CTAGGACTCCAGAGAAGGGATGGTGAAACCGAAGCTCGACTCTTCCAAACCATCTTGTTCAACTTCCCCATGTGTGC AAAAAAAAA

## FIGURE 1

Translation- 220 amino acids

MTSGEVKTSLKNAYSSAKRLSPKMEEEGEEEDYCTPGAFELERLFWKGSPQYTHVNEVWPKLYIGDEATALDRYRLQ KAGFTHVLNAAHGRWNVDTGPDYYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHSKILVHCVMGRSRS ATLVLAYLMIHKDMTLVDAIQQVAKNRCVLPNRGFLKQLRELDKQLVQQRRRSQRQDGEEEDGREL

FIGURE 2

100	DNLSGF DNLSGF DNLSGF DNLSR DNLSSH WEISSH PDISSH FNL		
90	PISOHUS PISOHUS PISOHUS PISOHUS PVEONUM PVEONHK PVEOSHT RANDIQEI RANDIQEI RANDIQEI RANDIQEI		
	EFKYKQI EFTYKQI OFHYKQI OFHYKQI ESRFIRV HYQYKSI HYQYKSI HLYKWI OITYKGI OITYKGI	183	
80	ALFENGG WFFEKNG WFFEKNG KP-DFIC KPFE-G WFFE-G WFFE-G WFFE-G WFYKDS	180183	ERTLGLSS ERTLGLSS ERTLGLSS ERSLRLE ERTLKLLH TQVLCH SQVLRPH SQVLRTS SQVLRTS SQVLRTS SQVLRTS SGVLRTS SGV
20	NLPNLFENGGEFYKQIPISDHASQNLSGF NLPNAFEHGGEFTYKQIPISDHASQNLSGF SCPKP-DFICESRFMRVPINDNYCEKLLPU SCPNHFEGLFHYKSIPVEDNAMVEISAN NCPNHFEGHYQYKSIPVEDNHKADISSN DCPNHFEGHYQYKSIPVEDNHKADISSN RTSEACHTHLHYKUIPVEDSHTADISSN SFMHVNTNANFYKDSGITYLGIKANDTQEFNLSRY RTSEACHTHLHYKUIPVEDSHTADISSN SFMHVNTNANFYKDSGITYLGIKANDTQEFNLSRY	170	FNFMGQLLDF FNFMGQLLDF FNFMGQLLDF FNFMGQLLQF SFMGQLLQF SFMGQLLQF SFMGQLLQF SFMGQLLQF GFFMGQLLQF FFFMGQLLQF FFFMGQLLQF FFFMGQLLQF
9	FPVEILPFLYLGCRKDSTNLDVLEEFGIKYILNVTPNLPNLFENGGEFKYKQIPISDHUSQNLSGF FPVEILPFLYLGCRKDSTNLDVLEFGIKYILNVTPNLPNFEHGGEFTYKQIPISDHUSQNLSGF FPVQILPNLYLGGRRDSTNLDVLGKYGIKYILNVTPNLPNFFEKNGGFHYKQIPISDHUSQNLSGF GLTRILPHLYLGSGRDSTNLESLRKLGIRYILNVTPSCPKP-DFICESRFHRVPINDNYCEKLLPU GPVEILPYLYLGSGRYHRSDLQGLQRCGITRVLNVSRSCPNHFEGLFHYKSIPVEDNUKRDISSH GPVEILPFLYLGSRYHRRDMLDRLGITRLINVSRDCPNHFEGHYQYKSIPVEDNHKRDISSH GPVEILPFLYLGSRYHRRDMLDRLGITRLINVSRDCPNHFEGHYQYKCIPVEDNHKRDISSH GPVEILPFLYLGSRYHRSKCEFLRNLHITRLLNVSRDCPNHFEGHYQYKCIPVEDNHKRDISSH GPVEILPFLYLGSRYHRSKCEFLRNLHITRLLNVSRRTSERCHTHLHYKUIPVEDSHTRDISSH HVNEVHPKLYIGDERTRLDRYRLQKLGITHVLNRREGRSFMHVNTNRNFYKDSGITYLGIKRNDTQEFNLSRY HVNEVHPKLYIGDERTRLDRYRLQKGITHVLNRREGRSFMHVNTNRNFYKDSGITYLGIKRNDTQEFNLSRY HVNEVHPKLYIGDERTRLDRYRLQKGFTHVLNRRHGRMNVDTGPDYYRDMDIQYHGVERDDLPTFDLSVF		SRSYTYTYAYLHQKLNLSHNDAYDIVKMKKSNISPNFNFHGQLLOFERTLGLSS SRSYTYTYAYLHQKHULSHNDAYDIVKMKKSNISPNFNFHGQLLOFERTLGLSS SRSYTYTYAYLHQKHLSLNDAYDLVKRKKSNISPNFNFHGQLLOFERTLGLSS SRSYTYTYAYLHQKLHLSLNDAYDLVKRKSNISPNFNFHGQLLOFERSLRLE SRSATIRIAYTHKTHGMSSDDAYRFVKDRRPSISPNFHHGQLLQFERSLRLE SRSATICLAYLHQSHRVRLDEAFDFVKQRRGVISPNFSFHGQLLQFESQVLCH SRSATICLAYLHKRKRVRLEEAFEFVKQRRSIISPNFSFHGQLLQFESQVLAPH SRSATICHAYLHKTKQFRLKEAFDYIKQRRSHVSPNFGFHGQLLQYESEILPSTP SRSPTLVTAYLHHKQMTLVDATQQVAKNRC-VLPNRGFLKQLRGLQYESTILPSTP SRSATLVTAYLHHKDMTLVDATQQVAKNRC-VLPNRGFLKQLRGLLQYESILPSTP SRSATLVTAYLHKDMTLVDATQQVAKNRC-VLPNRGFLKQLRGLLQYESILPSTP
	TNLDVLEFGI SANLESLAKLGI SANLESLAKLGI LUKDLHTQNGI SDLQGLQRCGI SSKCHLDRLGI ISKCEFLANLHI IQDIPKLQKLGI ILDRYKLQKRGF		LSMNDAYDIVKK LSLNDAYDIVKK LSLNDAYDLVKK MSSDDAYRFVKD WLDENFEFVKQ VKLDENFEFVKQ YRLEENFEFVKQ MTLYDAIQQYRK MJ.4AA!k.
	LYLGCRKDS: YLYLGCRKDS: NLYLGSRCNS: HLYLGSRCNY YLYLGSRYHR: FLYLGSRYHR: FLYLGSRYHR: FLYLGSRYHR: KLYLGGRYHR: KLYLGGRYHR: XLYLGGRYHR:		WAYLHOKINI WAYLHOKINI WAYLHOKINI IRYIHKTHGH LAYLHOKINI WAYLHKKKW HAYLHKKKW HAYLHKKKW WAYLHKKKW WAYLHKW
30		`	
20	DSDGSPLSNSQPS GRTPPPVGLRAS GRTPPPVGLRAS HSLSQPCLPVPSV ISSSCSTPLYDQG GCSSCGTPLHDQG VVNVSYRPRYDQG LSDGSGCYSLPSQ LERLFUKGSPQYT	120	KNCGVLVH GNCGVLVH GNCGVLVH SSCQVIVH GGGRVFVH CRGRVLVH KGGKVLVH KGGKVLVH MNGRVLVH
10	SOLDRO-PNSATESDGSPLSNSQPSI DRELPSSATESDGSPVPSSQPSI GRTPPPVGLRASI GLCEGKPARLLPHSLSQPCLPVPSV PAGALPPRGAENSNSOPRVPIYDQG PLSTSVPDSAESGCSSCSTPLYDQG PVPPSATEPLDLGCSSCGTPLHDQG SERALISQCGKPVVNSYRPAYDQG SGSFELSVQDLNDLLSDGSGCYSLPSQ	101 110	FPERISFIDER-RGKNCGVLVHCLRGI FPERISFIDER-RSKKCGVLVHCLRGI FPERIEFIDER-LSQNCGVLVHCLRGI LDKSIEFIDER-KISSCQVIVHCLRGI FQERISFIDSY-KNSGGRVLVHCQRGI FNERIDFIDSI-KNRGGRVFVHCQRGI FNERIDFIDCY-REKGGKVLVHCERGI FYPRARFIDRALSDDHSKILVHCWGR
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